



RECEIVED

JUN 26 2001

SEQUENCE LISTING

TECH CENTER 1600/2900

<110> McKeon, F.  
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Ryeom, S.

<120> CALCIPRESSINS: ENDOGENOUS INHIBITORS OF CALCINEURIN  
USES AND REAGENTS RELATED THERETO

<130> HMSU-P01-048

<140> 09/575,580  
<141> 2000-05-22

<160> 45

<170> PatentIn Ver. 2.1

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35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala  
50 55 60

Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu  
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu  
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser  
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn  
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr  
130 135 140

Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val  
145 150 155 160

Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg  
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Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr  
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Thr Pro Ile His Leu Ser  
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Arg Asp Trp Ala Val Thr Gln Cys Phe Ala Glu Glu Ala Phe Gln Ala  
35 40 45

Leu Thr Asp Phe Ser Asp Leu Pro Asn Ser Leu Phe Ala Cys Asn Val  
50 55 60

His Gln Ser Val Phe Glu Glu Glu Ser Lys Glu Lys Phe Glu Gly  
65 70 75 80

Leu Phe Arg Thr Tyr Asp Glu Cys Val Thr Phe Gln Leu Phe Lys Ser  
85 90 95

Phe Arg Arg Val Arg Ile Asn Phe Ser His Pro Lys Ser Ala Ala Arg  
100 105 110

Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Pro  
115 120 125

Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu  
130 135 140

His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro  
145 150 155 160

Ser Ser Pro Ser Val Gly Trp Lys Pro Ile Ser Asp Ala Thr Pro Val  
165 170 175

Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu  
180 185 190

Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val  
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His Val Cys Asp Ser Asp Met Glu Arg Glu Glu Asp Pro Lys Thr Ser  
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Pro Lys Pro Lys Ile Asn Gln Thr Arg Arg Pro Gly Leu Pro Pro Phe  
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<213> Homo sapiens

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Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg  
35 40 45

Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile  
50 55 60

Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe  
65 70 75 80

Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala  
85 90 95

Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro  
100 105 110

Pro Val Gly Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr  
115 120 125

Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu  
130 135 140

Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys  
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Asp Ser Asp Ile Glu Glu Glu Asp Pro Lys Thr Ser Pro Lys Pro  
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Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro Pro Ser Val Ser Asn  
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Ser Asn Pro Phe Ser Ala Ala Asp Ala Arg Leu Gln Leu His Lys Thr  
35 40 45

Glu Phe Leu Gly Lys Glu Met Lys Leu Tyr Phe Ala Gln Thr Leu His  
50 55 60

Ile Gly Ser Ser His Leu Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu  
65 70 75 80

Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Val Glu Asp  
85 90 95

Ala Thr Pro Val Ile Asn Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu  
100 105 110

Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Ala Thr Asp Thr Thr Pro  
115 120 125

Ser Val Val Val His Val Cys Glu Ser Asp Gln Glu Lys Glu Glu

130                    135                    140  
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Arg Arg Pro Glu Tyr Thr Pro Ile His Leu  
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<213> Cricetulus griseus  
  
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Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe  
35                    40                    45  
Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala  
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Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu  
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Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu  
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Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser  
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Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn  
115                    120                    125  
Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr  
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Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val  
145                    150                    155                    160  
Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Met Glu Arg Met  
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Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr  
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Pro Ile His Leu Ser  
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<213> Caenorhabditis elegans

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Ile Val Thr Gln Val Pro Glu Asp Val Phe Asp Asn Lys Gln Asp Lys  
35 40 45

Ala Asn Phe Ser Ser Leu Phe Thr Gln Ile Glu Lys Asp Ile His Phe  
50 55 60

Asp Phe Leu Arg Ser Phe Arg Arg Val Arg Val Ile Phe Ser Ser Pro  
65 70 75 80

Glu Asn Ala Thr Ala Ala Lys Leu Ile Val Gln Gly Phe Ser Phe Lys  
85 90 95

Gly His Glu Leu Lys Ala Phe Phe Ala Gln Arg Ile Tyr Met Ser Ala  
100 105 110

Asn Ser Gln Met Leu Ser Pro Pro Pro Leu Glu Lys Gln Phe Leu Ile  
115 120 125

Ser Pro Pro Cys Ser Pro Pro Val Gly Trp Glu Gln Thr Lys Asp Met  
130 135 140

Pro Pro Val Val Cys Asn Phe Asp Leu Met Ala Arg Leu Ala Ser Phe  
145 150 155 160

Ala Ile Asp Glu Lys Tyr Glu Val His Asn Gly Asp Glu Leu Thr Pro  
165 170 175

Ala Ile Ile Val His Pro Cys Glu Thr Pro Ile Asp Val Pro Ser Ala  
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<213> Saccharomyces cerevisiae

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Lys Asn Ile Leu Arg Lys Phe Gln Ile Asn Glu Asn Glu Pro Leu Gln

35                    40                    45

Leu Ile Ile Leu Lys Arg Phe Lys Arg Ile Leu Leu Ile Cys Pro Ser  
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His Asp Ile Ser Gln His Val Met Asp Ala Ser Arg Ala Leu Glu Met  
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Glu Asn Phe Asn Phe Ser Tyr Ser Leu Gln Asp Gly Gln Arg Asn Leu  
85                    90                    95

Thr Lys Gln Tyr Leu Lys Val Pro Glu Ser Glu Lys Met Phe Leu Ile  
100                  105                  110

Ser Pro Pro Ala Ser Pro Pro Glu Phe Asp Phe Ser Lys Cys Glu  
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Asp Ala Pro Gln Arg His Ile Gln Ser His Ile Gln Gln Asp Gln Gln  
130                  135                  140

Gln Arg Leu Glu Ala Ser Gln Leu Leu Pro Asn Asn Pro Asp Lys Asn  
145                  150                  155                  160

Asn Asn Gly Thr Phe Thr Leu Leu Lys Ser Lys Val Gly Ala Ile Thr  
165                  170                  175

Ile Asp Arg Cys Pro Thr Asn Asp Gly Asn Gly Gln Met Gln Leu Ala  
180                  185                  190

Asp His Val Lys Thr Ala Phe Pro Pro Lys Ser Ile Phe Asp Thr Asp  
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Asp Asp Asp  
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Leu Gly Lys Val Leu Ala Ser Tyr Asn Asp Lys Ala Val Glu Glu Asp  
35                  40                  45

Thr Leu Lys Lys Ser Ser Thr Gly Ser Leu Pro Ser Gly Gln Gln Val  
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His Cys Gln Tyr Val Leu Asp Asp Pro Asn His Val Glu Gly Ile Ser  
65                  70                  75                  80

Val Asp Gln Ser Leu Gln Val Pro Lys Phe Glu Lys Asn Trp Leu Ile  
85 90 95

Ser Pro Pro Gly Ser Pro Pro Val Gly Trp Glu Pro Ile Val Glu Glu  
100 105 110

Ser Pro Asn Ser Gln His Leu Ala His Asp Ile Gln Leu Lys Leu Asp  
115 120 125

Glu Leu Gly Asn Ala Leu Leu Asn Asp His Ser Ala Gly Pro Gln Ile  
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Phe Glu His

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35 40 45

Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Val Gln Glu Gln  
50 55 60

Lys Glu Arg Phe Glu Ala Leu Phe Thr Leu Tyr Asp Asp Gln Val Thr  
65 70 75 80

Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys  
85 90 95

Pro Ala Arg Ala Arg Ile Glu Leu His Glu Ser Glu Phe His Gly Arg  
100 105 110

Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Val Ser Gly Glu Ala Arg  
115 120 125

Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Thr Lys Gln Phe Leu Ile  
130 135 140

Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser Glu Asp Ala  
145 150 155 160

Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser Lys Leu Gly  
165 170 175

Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser  
180 185 190

Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu Asp Thr  
195 200 205

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<210> 26  
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<212> DNA  
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<210> 27  
<211> 3717  
<212> DNA  
<213> Mus musculus

<220>  
<221> modified base  
<222> (1)..(3717)  
<223> n=a, c, g, or t

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<210> 28

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: general structure

<220>

<221> SITE

<222> (6)

<223> Xaa=any amino acid residue

<400> 28

Pro Lys Pro Lys Ile Xaa Gln Thr Arg Arg Pro Glu

1

5

10

<210> 29

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: calcineurin

antagonist

<400> 29  
Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu  
1 5 10

<210> 30  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: calcineurin antagonist

<400> 30  
Pro Lys Pro Lys Ile Asn Gln Thr Arg Arg Pro Gly  
1 5 10

<210> 31  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: EGF-derived peptide

<400> 31  
Cys Met His Ile Glu Ser Leu Asp Ser Tyr Thr Cys  
1 5 10

<210> 32  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: EGF-derived peptide

<400> 32  
Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys  
1 5 10

<210> 33  
<211> 32  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: pH-dependent membrane-binding internalizing peptide

<220>  
<221> SITE  
<222> (1)  
<223> Xaa=preferably a unique residue, such as Cys or Lys, that facilitates chemical conjugation of the internalizing peptide to a targeting protein conjugate

<220>  
<221> SITE  
<222> (2)..(3)  
<223> Xaa=residues selected to modulate the affinity of the internalizing peptide for different membranes

<400> 33  
Xaa Xaa Xaa Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala  
1 5 10 15  
  
Glu Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala  
20 25 30

<210> 34  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide substrate

<400> 34  
Gly Asn Ala Ala Ala Ala Arg Arg  
1 5

<210> 35  
<211> 75  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> CDS  
<222> (4)..(75)

<220>  
<223> Description of Artificial Sequence: synthetic construct

<400> 35  
cat atg ggt ggc tgc cgt ggc gat atg ttc ggt tgc ggt gct cct cca 48  
Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro  
1 5 10 15

aaa aag aag aga aag gta gct gga ttc  
Lys Lys Lys Arg Lys Val Ala Gly Phe  
20

75

<210> 36  
<211> 24  
<212> PRT  
<213> Artificial Sequence  
<223> Description of Artificial Sequence: synthetic construct

<400> 36  
Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro Lys  
1 5 10 15  
Lys Lys Arg Lys Val Ala Gly Phe  
20

<210> 37  
<211> 225  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: synthetic construct  
  
<220>  
<221> CDS  
<222> (4)..(225)

<400> 37  
cat atg gag cca gta gat cct aga cta gag ccc tgg aag cat cca gga 48  
Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly  
1 5 10 15

agt cag cct aaa act gct tgt acc aat tgc tat tgt aaa aag tgt tgc 96  
Ser Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Cys Cys  
20 25 30

ttt cat tgc caa gtt tgt ttc ata aca aaa gcc ctt ggc atc tcc tat 144  
Phe His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr  
35 40 45

ggc agg aag aag cgg aga cag cga cga aga cct cct caa ggc agt cag 192  
Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln  
50 55 60

act cat caa gtt tct cta agt aag caa gga ttc 225  
Thr His Gln Val Ser Leu Ser Lys Gln Gly Phe  
65 70

<210> 38  
<211> 74  
<212> PRT  
<213> Artificial Sequence  
<223> Description of Artificial Sequence: synthetic construct

<400> 38  
Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser  
1 5 10 15  
  
Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe  
20 25 30  
  
His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly  
35 40 45  
  
Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr  
50 55 60  
  
His Gln Val Ser Leu Ser Lys Gln Gly Phe  
65 70

<210> 39  
<211> 912  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: synthetic construct

<220>  
<221> CDS  
<222> (4)..(912)

<400> 39  
cat atg acc tct cgc cgc tcc gtg aag tcg ggt ccg cg<sup>48</sup>  
Met Thr Ser Arg Arg Ser Val Lys Ser Gly Pro Arg Glu Val Pro  
1 5 10 15  
  
cgc gat gag tac gag gat ctg tac tac acc ccg tct tca ggt atg g<sup>96</sup>  
Arg Asp Glu Tyr Glu Asp Leu Tyr Tyr Thr Pro Ser Ser Gly Met Ala  
20 25 30  
  
agt ccc gat agt ccg cct gac acc tcc cgc cgt ggc gcc cta cag aca  
Ser Pro Asp Ser Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr  
35 40 45  
  
cgc tcg cgc cag agg ggc gag gtc cgt ttc gtc cag tac gac gag tcg  
Arg Ser Arg Gln Arg Gly Glu Val Arg Phe Val Gln Tyr Asp Glu Ser  
50 55 60  
  
gat tat gcc ctc tac ggg ggc tcg tca tcc gaa gac gac gaa cac ccg  
Asp Tyr Ala Leu Tyr Gly Ser Ser Glu Asp Asp Glu His Pro  
240

65	70	75	
gag gtc ccc cgg acg cgg cgt ccc gtt tcc	ggg gcg gtt ttg tcc	ggc	288
Glu Val Pro Arg Thr Arg Arg Pro Val Ser	Gly Ala Val Leu Ser	Gly	
80	85	90	95
ccg ggg cct gcg cgg gcg cct ccg cca ccc	gct ggg tcc gga ggg gcc		336
Pro Gly Pro Ala Arg Ala Pro Pro Pro	Ala Gly Ser Gly Gly Ala		
100	105		110
gga cgc aca ccc acc acc gcc ccc cgg	gcc ccc cga acc cag cgg gtg		384
Gly Arg Thr Pro Thr Ala Pro Arg	Ala Pro Arg Thr Gln Arg Val		
115	120		125
gcg act aag gcc ccc gcg gcc ccg	gag acc acc cgc ggc agg		432
Ala Thr Lys Ala Pro Ala Ala Pro Ala	Glu Thr Thr Arg Gly Arg		
130	135		140
aaa tcg gcc cag cca gaa tcc gcc	gca ctc cca gac gcc ccc gcg tcg		480
Lys Ser Ala Gln Pro Glu Ser Ala	Ala Leu Pro Asp Ala Pro Ala Ser		
145	150		155
acg gcg cca acc cga tcc aag aca ccc	gcg cag ggg ctg gcc aga aag		528
Thr Ala Pro Thr Arg Ser Lys Thr Pro	Ala Gln Gly Leu Ala Arg Lys		
160	165		175
ctg cac ttt agc acc gcc ccc	cca aac ccc gac gcg cca tgg acc ccc		576
Leu His Phe Ser Thr Ala Pro	Pro Asn Pro Asp Ala Pro Trp Thr Pro		
180	185		190
cgg gtg gcc ggc ttt aac aag	cgc gtc ttc tgc gcc gcg gtc		624
Arg Val Ala Gly Phe Asn Lys Arg	Val Phe Cys Ala Ala Val Gly Arg		
195	200		205
ctg gcg gcc atg cat gcc cgg	atg gcg gcg gtc cag ctc tgg gac atg		672
Leu Ala Ala Met His Ala Arg	Met Ala Ala Val Gln Leu Trp Asp Met		
210	215		220
tcg cgt ccg cgc aca gac	gaa gac ctc aac gaa ctc ctt ggc atc acc		720
Ser Arg Pro Arg Thr Asp	Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr		
225	230		235
acc atc cgc gtg acg gtc	tgc gag ggc aaa aac ctg ctt cag cgc gcc		768
Thr Ile Arg Val Thr Val	Cys Glu Gly Lys Asn Leu Leu Gln Arg Ala		
240	245		255
aac gag ttg gtg aat cca	gac gtg gtg cag gac gtc gac gcg gcc acg		816
Asn Glu Leu Val Asn Pro	Asp Val Val Gln Asp Val Asp Ala Ala Thr		
260	265		270
gcg act cga ggg cgt tct	gcg gcg tcg cgc ccc acc gag cga cct cga		864
Ala Thr Arg Gly Arg Ser Ala Ala Ser	Arg Pro Thr Glu Arg Pro Arg		
275	280		285
gcc cca gcc cgc tcc	gtt tct cgc ccc aga cgg ccc gtc gag gaa ttc		912
Ala Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val	Glu Glu Phe		

290

295

300

<210> 40

<211> 303

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: synthetic  
construct

<400> 40

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1 5 10 15

Asp Glu Tyr Glu Asp Leu Tyr Tyr Thr Pro Ser Ser Gly Met Ala Ser  
20 25 30

Pro Asp Ser Pro Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr Arg  
35 40 45

Ser Arg Gln Arg Gly Glu Val Arg Phe Val Gln Tyr Asp Glu Ser Asp  
50 55 60

Tyr Ala Leu Tyr Gly Gly Ser Ser Ser Glu Asp Asp Glu His Pro Glu  
65 70 75 80

Val Pro Arg Thr Arg Arg Pro Val Ser Gly Ala Val Leu Ser Gly Pro  
85 90 95

Gly Pro Ala Arg Ala Pro Pro Pro Pro Ala Gly Ser Gly Gly Ala Gly  
100 105 110

Arg Thr Pro Thr Thr Ala Pro Arg Ala Pro Arg Thr Gln Arg Val Ala  
115 120 125

Thr Lys Ala Pro Ala Ala Pro Ala Ala Glu Thr Thr Arg Gly Arg Lys  
130 135 140

Ser Ala Gln Pro Glu Ser Ala Ala Leu Pro Asp Ala Pro Ala Ser Thr  
145 150 155 160

Ala Pro Thr Arg Ser Lys Thr Pro Ala Gln Gly Leu Ala Arg Lys Leu  
165 170 175

His Phe Ser Thr Ala Pro Pro Asn Pro Asp Ala Pro Trp Thr Pro Arg  
180 185 190

Val Ala Gly Phe Asn Lys Arg Val Phe Cys Ala Ala Val Gly Arg Leu  
195 200 205

Ala Ala Met His Ala Arg Met Ala Ala Val Gln Leu Trp Asp Met Ser  
210 215 220

Arg Pro Arg Thr Asp Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr Thr  
225 230 235 240

Ile Arg Val Thr Val Cys Glu Gly Lys Asn Leu Leu Gln Arg Ala Asn

245                    250                    255  
Glu Leu Val Asn Pro Asp Val Val Gln Asp Val Asp Ala Ala Thr Ala  
260                    265                    270  
Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr Glu Arg Pro Arg Ala  
275                    280                    285  
Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val Glu Glu Phe  
290                    295                    300

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<220>  
<223> Description of Artificial Sequence: synthetic  
construct

<220>  
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Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala  
1                        5                            10                        15  
  
tcg cgc ccc acc gag cga cct cga gcc cca gcc cgc tcc gct tct cgc    96  
Ser Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg  
20                        25                            30  
  
ccc aga cgg ccc gtc gag gaa ttc    120  
Pro Arg Arg Pro Val Glu Glu Phe  
35

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<212> PRT  
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<400> 42    42  
Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser  
1                        5                            10                        15  
  
Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro  
20                        25                            30  
  
Arg Arg Pro Val Glu Glu Phe  
35

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<211> 15  
<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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15

<210> 44  
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<213> Mus musculus

<400> 44  
Glu Arg Met Arg Arg Pro  
1 5

<210> 45  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
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sequence

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Glu Arg Met Pro Pro Arg Arg Asp  
1 5

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Cont